- - **Figure 2:** (A) Schematic representation of a leucine zipper pair visualized from the *N*-terminus illustrating e/g-interactions and the hydrophobic core formed by the a- and d-positions. (B) Distribution of residues at the semi-randomized positions throughout selection. The number of zipper pairs sequenced is given in parentheses, save "Before selection" where the theoretical distribution is reported. Each pair carries one core a-pair and 6 e/g-pairs. Neutral e/g-pairs have one or both residues as Gln. In "Competition (I114A)" only clones from P6 to P12 (not from earlier passages) were considered for analysis. Thus, 37 individual clones were identified, giving rise to 10 unique sequences due to multiple occurrence of the enriched clones. The distributions were calculated according to the frequency of sequence occurrence (n=37). (C) Leucine zipper sequences WinZip-A1 (SEQ ID NO:1), WinZip-B1 (SEQ ID NO:2), WinZip-A2 (SEQ ID NO:3) and WinZip-B2 (SEQ ID NO:4) obtained after competition selection and chain shuffling. The heptad positions (*a* to *g*) are followed by the heptad number (1 to 5). Invariant residues from GCN4 are underlined. Clear boxes indicate the semi-randomized e- and g-positions (black outline) and core a-position (a3) (grey outline). Circled residues were designed to contribute to helix capping. Shaded residues were designed for the introduction of restriction sites. Other residues are from c-Jun (LibA) or c-Fos (LibB). Arrows indicate putative e/g-interactions. –

## REMARKS

The above amendment is presented in compliance with 37 C.F.R. 1.821(d), namely to introduce sequence identifiers for the four designed peptide sequences shown in Figure 2(C). The amendment also inserts the name abbreviations for each of